



Rec'd PCT/PTO 29 APR 2005

Docket No.: 13111-00001-US

10/521916 (AGENT)

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Patent Application of:  
Markus Matuschek et al.

Application No.: 10/521,916

Confirmation No.: N/A

Filed: January 20, 2005

Art Unit: N/A

For: PROCESS FOR THE BIOTRANSFORMATION  
OF CAROTENOIDS

Examiner: Not Yet Assigned

**STATEMENT TO SUPPORT FILING AND SUBMISSION  
IN ACCORDANCE WITH 37 CFR §§1.821 THROUGH 1.825**

MS Sequence  
Commissioner for Patents  
P.O. Box 1450  
Alexandria, VA 22313-1450

Dear Sir:

- ☐ I hereby state, in accordance with the requirements of **37 C.F.R. §1.821(f)**, that the information recorded in computer readable form is identical to the written Sequence Listing submitted herewith.
- ☐ I hereby state that the submission filed in accordance with **37 C.F.R. 1.821(g)** does not include new matter.
- ☐ I hereby state that the submission filed in accordance with **37 C.F.R. §1.821(h)** does not include new matter or go beyond the disclosure in the international application as filed.
- ☒ I hereby state that the amendments, made in accordance with **37 C.F.R. §1.825(a)**, included in the substitute sheet(s) of the Sequence Listing are supported in the application, as filed, in pages 1-11 of the Sequence Listing. I hereby state that the substitute sheets of the Sequence Listing do not include new matter.
- ☒ I hereby state that the substitute copy of the computer readable form, submitted in accordance with **37 C.F.R. §1.825(b)**, is the same as the amended Sequence Listing.
- ☐ I hereby state that the substitute copy of the computer readable form, submitted in accordance with **37 C.F.R. §1.825(d)**, contains identical data to that originally filed on January 20, 2005.

Application No.: 10/521916

Docket No.: 13111-00001-US

Dated: *April 26, 2005*

Respectfully submitted,

By *Christine M. Hansen*

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10/521916

SEQUENCE LISTING

<110> Matuschek, Markus  
Hauer, Bernhard  
Schmid, Rolf  
Kauffmann, Isabelle  
Blasco, Francesca  
Schmidt-Dannert, Claudia

<120> Process for the biotransformation of carotenoids

<130> 13111-00001-US

<140> 10/521,916

<141> 2005-01-20

<150> PCT/EP2003/008199

<151> 2003-07-25

<150> DE 102 34 126.5

<151> 2002-07-26

<160> 12

<170> PatentIn Ver. 3.3

<210> 1

<211> 1170

<212> DNA

<213> *Thermus thermophilus*

<220>

<221> CDS

<222> (1) .. (1170)

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Met	Lys	Arg	Leu	Ser	Leu	Arg	Glu	Ala	Trp	Pro	Tyr	Leu	Lys	Asp	Leu	
1				5				10					15			

cag	caa	gat	ccc	ctc	gcc	gtc	ctg	ctg	gcg	tgg	ggc	cgg	gcc	cac	ccc	96
Gln	Gln	Asp	Pro	Leu	Ala	Val	Leu	Leu	Ala	Trp	Gly	Arg	Ala	His	Pro	
		20					25				30					

cgg	ctc	ttc	ctt	ccc	ctg	ccc	cgc	ttc	ccc	ctg	gcc	ctg	atc	ttt	gac	144
Arg	Leu	Phe	Leu	Pro	Leu	Pro	Arg	Phe	Pro	Leu	Ala	Leu	Ile	Phe	Asp	
		35					40				45					

ccc	gag	ggg	gtg	gag	ggg	gcg	ctc	ctc	gcc	gag	ggg	acc	acc	aag	gcc	192
Pro	Glu	Gly	Val	Glu	Gly	Ala	Leu	Leu	Ala	Glu	Gly	Thr	Thr	Lys	Ala	
	50					55				60						

acc ttc cag tac cgg gcc ctc tcc cgc ctc acg ggg agg ggc ctc ctc	240
Thr Phe Gln Tyr Arg Ala Leu Ser Arg Leu Thr Gly Arg Gly Leu Leu	
65 70 75 80	
acc gac tgg ggg gaa agc tgg aag gag gcg cgc aag gcc ctc aaa gac	288
Thr Asp Trp Gly Glu Ser Trp Lys Glu Ala Arg Lys Ala Leu Lys Asp	
85 90 95	
ccc ttc ctg ccg aag aac gtc cgc ggc tac cgg gag gcc atg gag gag	336
Pro Phe Leu Pro Lys Asn Val Arg Gly Tyr Arg Glu Ala Met Glu Glu	
100 105 110	
gag gcc cgg gcc ttc ttc ggg gag tgg cgg ggg gag gag cgg gac ctg	384
Glu Ala Arg Ala Phe Phe Gly Glu Trp Arg Gly Glu Glu Arg Asp Leu	
115 120 125	
gac cac gag atg ctc gcc ctc tcc ctg cgc ctc ctc ggg cgg gcc ctc	432
Asp His Glu Met Leu Ala Leu Ser Leu Arg Leu Leu Gly Arg Ala Leu	
130 135 140	
ttc ggg aag ccc ctc tcc cca agc ctc gcg gag cac gcc ctt aag gcc	480
Phe Gly Lys Pro Leu Ser Pro Ser Leu Ala Glu His Ala Leu Lys Ala	
145 150 155 160	
ctg gac cgg atc atg gcc cag acc agg agc ccc ctg gcc ctc ctg gac	528
Leu Asp Arg Ile Met Ala Gln Thr Arg Ser Pro Leu Ala Leu Leu Asp	
165 170 175	
ctg gcc gcc gaa gcc cgc ttc cgg aag gac cgg ggg gcc ctc tac cgc	576
Leu Ala Ala Glu Ala Arg Phe Arg Lys Asp Arg Gly Ala Leu Tyr Arg	
180 185 190	
gag gcg gaa gcc ctc atc gtc cac ccg ccc ctc tcc cac ctt ccc cga	624
Glu Ala Glu Ala Leu Ile Val His Pro Pro Leu Ser His Leu Pro Arg	
195 200 205	
gag cgc gcc ctg agc gag gcc gtg acc ctc ctg gtg gcg ggc cac gag	672
Glu Arg Ala Leu Ser Glu Ala Val Thr Leu Leu Val Ala Gly His Glu	
210 215 220	
acg gtg gcg agc gcc ctc acc tgg tcc ttt ctc ctc ctc tcc cac cgc	720
Thr Val Ala Ser Ala Leu Thr Trp Ser Phe Leu Leu Leu Ser His Arg	
225 230 235 240	
ccg gac tgg cag aag cgg gtg gcc gag agc gag gag gcg gcc ctc gcc	768
Pro Asp Trp Gln Lys Arg Val Ala Glu Ser Glu Glu Ala Ala Leu Ala	
245 250 255	
gcc ttc cag gag gcc ctg agg ctc tac ccc ccc gcc tgg atc ctc acc	816
Ala Phe Gln Glu Ala Leu Arg Leu Tyr Pro Pro Ala Trp Ile Leu Thr	
260 265 270	
cgg agg ctg gaa agg ccc ctc ctc ctg gga gag gac cgg ctc ccc ccg	864
Arg Arg Leu Glu Arg Pro Leu Leu Leu Gly Glu Asp Arg Leu Pro Pro	
275 280 285	
ggc acc acc ctg gtc ctc tcc ccc tac gtg acc cag agg ctc cac ttc	912

Gly Thr Thr Leu Val Leu Ser Pro Tyr Val Thr Gln Arg Leu His Phe  
 290 295 300  
 ccc gat ggg gag gcc ttc cgg ccc gag cgc ttc ctg gag gaa agg ggg 960  
 Pro Asp Gly Glu Ala Phe Arg Pro Glu Arg Phe Leu Glu Glu Arg Gly  
 305 310 315 320  
 acc cct tcg ggg cgc tac ttc ccc ttt ggc ctg ggg cag agg ctc tgc 1008  
 Thr Pro Ser Gly Arg Tyr Phe Pro Phe Gly Leu Gly Gln Arg Leu Cys  
 325 330 335  
 ctg ggg cgg gac ttc gcc ctc ctc gag ggc ccc atc gtc ctc agg gcc 1056  
 Leu Gly Arg Asp Phe Ala Leu Leu Glu Gly Pro Ile Val Leu Arg Ala  
 340 345 350  
 ttc ttc cgc cgc ttc cgc cta gac ccc ctc ccc ttc ccc cgg gtc ctc 1104  
 Phe Phe Arg Arg Phe Arg Leu Asp Pro Leu Pro Phe Pro Arg Val Leu  
 355 360 365  
 gcc cag gtc acc ctg agg ccc gaa ggc ggg ctt ccc gcg cgg cct agg 1152  
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 370 375 380  
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<211> 389

<212> PRT

<213> Thermus thermophilus

<400> 2

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 Arg Leu Phe Leu Pro Leu Pro Arg Phe Pro Leu Ala Leu Ile Phe Asp  
 35 40 45  
 Pro Glu Gly Val Glu Gly Ala Leu Leu Ala Glu Gly Thr Thr Lys Ala  
 50 55 60  
 Thr Phe Gln Tyr Arg Ala Leu Ser Arg Leu Thr Gly Arg Gly Leu Leu  
 65 70 75 80  
 Thr Asp Trp Gly Glu Ser Trp Lys Glu Ala Arg Lys Ala Leu Lys Asp  
 85 90 95  
 Pro Phe Leu Pro Lys Asn Val Arg Gly Tyr Arg Glu Ala Met Glu Glu  
 100 105 110

Glu Ala Arg Ala Phe Phe Gly Glu Trp Arg Gly Glu Glu Arg Asp Leu  
 115 120 125  
 Asp His Glu Met Leu Ala Leu Ser Leu Arg Leu Leu Gly Arg Ala Leu  
 130 135 140  
 Phe Gly Lys Pro Leu Ser Pro Ser Leu Ala Glu His Ala Leu Lys Ala  
 145 150 155 160  
 Leu Asp Arg Ile Met Ala Gln Thr Arg Ser Pro Leu Ala Leu Leu Asp  
 165 170 175  
 Leu Ala Ala Glu Ala Arg Phe Arg Lys Asp Arg Gly Ala Leu Tyr Arg  
 180 185 190  
 Glu Ala Glu Ala Leu Ile Val His Pro Pro Leu Ser His Leu Pro Arg  
 195 200 205  
 Glu Arg Ala Leu Ser Glu Ala Val Thr Leu Leu Val Ala Gly His Glu  
 210 215 220  
 Thr Val Ala Ser Ala Leu Thr Trp Ser Phe Leu Leu Leu Ser His Arg  
 225 230 235 240  
 Pro Asp Trp Gln Lys Arg Val Ala Glu Ser Glu Glu Ala Ala Leu Ala  
 245 250 255  
 Ala Phe Gln Glu Ala Leu Arg Leu Tyr Pro Pro Ala Trp Ile Leu Thr  
 260 265 270  
 Arg Arg Leu Glu Arg Pro Leu Leu Leu Gly Glu Asp Arg Leu Pro Pro  
 275 280 285  
 Gly Thr Thr Leu Val Leu Ser Pro Tyr Val Thr Gln Arg Leu His Phe  
 290 295 300  
 Pro Asp Gly Glu Ala Phe Arg Pro Glu Arg Phe Leu Glu Glu Arg Gly  
 305 310 315 320  
 Thr Pro Ser Gly Arg Tyr Phe Pro Phe Gly Leu Gly Gln Arg Leu Cys  
 325 330 335  
 Leu Gly Arg Asp Phe Ala Leu Leu Glu Gly Pro Ile Val Leu Arg Ala  
 340 345 350  
 Phe Phe Arg Arg Phe Arg Leu Asp Pro Leu Pro Phe Pro Arg Val Leu  
 355 360 365  
 Ala Gln Val Thr Leu Arg Pro Glu Gly Gly Leu Pro Ala Arg Pro Arg  
 370 375 380  
 Glu Glu Val Arg Ala  
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<211> 1188

<212> DNA

<213> Artificial sequence

<220>

<221> misc\_feature

<222> (4)..(21)

<223> His tag

<220>

<223> Description of the artificial sequence: N-terminal  
his tagged

<220>

<221> CDS

<222> (1)..(1188)

<400> 3

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Pro Tyr Leu Lys Asp Leu Gln Gln Asp Pro Leu Ala Val Leu Leu Ala	
20 25 30	
tgg ggc cgg gcc cac ccc cgg ctc ttc ctt ccc ctg ccc cgc ttc ccc	144
Trp Gly Arg Ala His Pro Arg Leu Phe Leu Pro Leu Pro Arg Phe Pro	
35 40 45	
ctg gcc ctg atc ttt gac ccc gag ggg gtg gag ggg gcg ctc ctc gcc	192
Leu Ala Leu Ile Phe Asp Pro Glu Gly Val Glu Gly Ala Leu Leu Ala	
50 55 60	
gag ggg acc acc aag gcc acc ttc cag tac cgg gcc ctc tcc cgc ctc	240
Glu Gly Thr Thr Lys Ala Thr Phe Gln Tyr Arg Ala Leu Ser Arg Leu	
65 70 75 80	
acg ggg agg ggc ctc ctc acc gac tgg ggg gaa agc tgg aag gag gcg	288
Thr Gly Arg Gly Leu Leu Thr Asp Trp Gly Glu Ser Trp Lys Glu Ala	
85 90 95	
cgc aag gcc ctc aaa gac ccc ttc ctg ccg aag aac gtc cgc ggc tac	336
Arg Lys Ala Leu Lys Asp Pro Phe Leu Pro Lys Asn Val Arg Gly Tyr	
100 105 110	
cgg gag gcc atg gag gag gag gcc cgg gcc ttc ttc ggg gag tgg cgg	384
Arg Glu Ala Met Glu Glu Glu Ala Arg Ala Phe Phe Gly Glu Trp Arg	

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ctc ctc ggg cgg gcc ctc ttc ggg aag ccc ctc tcc cca agc ctc gcg Leu Leu Gly Arg Ala Leu Phe Gly Lys Pro Leu Ser Pro Ser Leu Ala 145 150 155 160			480
gag cac gcc ctt aag gcc ctg gac cgg atc atg gcc cag acc agg agc Glu His Ala Leu Lys Ala Leu Asp Arg Ile Met Ala Gln Thr Arg Ser 165 170 175			528
ccc ctg gcc ctc ctg gac ctg gcc gcc gaa gcc cgc ttc cgg aag gac Pro Leu Ala Leu Leu Asp Leu Ala Ala Glu Ala Arg Phe Arg Lys Asp 180 185 190			576
cgg ggg gcc ctc tac cgc gag gcg gaa gcc ctc atc gtc cac ccg ccc Arg Gly Ala Leu Tyr Arg Glu Ala Glu Ala Leu Ile Val His Pro Pro 195 200 205			624
ctc tcc cac ctt ccc cga gag cgc gcc ctg agc gag gcc gtg acc ctc Leu Ser His Leu Pro Arg Glu Arg Ala Leu Ser Glu Ala Val Thr Leu 210 215 220			672
ctg gtg gcg ggc cac gag acg gtg gcg agc gcc ctc acc tgg tcc ttt Leu Val Ala Gly His Glu Thr Val Ala Ser Ala Leu Thr Trp Ser Phe 225 230 235 240			720
ctc ctc ctc tcc cac cgc ccg gac tgg cag aag cgg gtg gcc gag agc Leu Leu Leu Ser His Arg Pro Asp Trp Gln Lys Arg Val Ala Glu Ser 245 250 255			768
gag gag gcg gcc ctc gcc gcc ttc cag gag gcc ctg agg ctc tac ccc Glu Glu Ala Ala Leu Ala Ala Phe Gln Glu Ala Leu Arg Leu Tyr Pro 260 265 270			816
ccc gcc tgg atc ctc acc cgg agg ctg gaa agg ccc ctc ctc ctg gga Pro Ala Trp Ile Leu Thr Arg Arg Leu Glu Arg Pro Leu Leu Leu Gly 275 280 285			864
gag gac cgg ctc ccc ccg ggc acc acc ctg gtc ctc tcc ccc tac gtg Glu Asp Arg Leu Pro Pro Gly Thr Thr Leu Val Leu Ser Pro Tyr Val 290 295 300			912
acc cag agg ctc cac ttc ccc gat ggg gag gcc ttc cgg ccc gag cgc Thr Gln Arg Leu His Phe Pro Asp Gly Glu Ala Phe Arg Pro Glu Arg 305 310 315 320			960
ttc ctg gag gaa agg ggg acc cct tcg ggg cgc tac ttc ccc ttt ggc Phe Leu Glu Glu Arg Gly Thr Pro Ser Gly Arg Tyr Phe Pro Phe Gly 325 330 335			1008
ctg ggg cag agg ctc tgc ctg ggg cgg gac ttc gcc ctc ctc gag ggc Leu Gly Gln Arg Leu Cys Leu Gly Arg Asp Phe Ala Leu Leu Glu Gly 340 345 350			1056



ccc atc gtc ctc agg gcc ttc ttc cgc cgc ttc cgc cta gac ccc ctc 1104  
Pro Ile Val Leu Arg Ala Phe Phe Arg Arg Phe Arg Leu Asp Pro Leu  
355 360 365

ccc ttc ccc cgg gtc ctc gcc cag gtc acc ctg agg ccc gaa ggc ggg 1152  
Pro Phe Pro Arg Val Leu Ala Gln Val Thr Leu Arg Pro Glu Gly Gly  
370 375 380

ctt ccc gcg cgg cct agg gag gag gtg cgg gcg tga 1188  
Leu Pro Ala Arg Pro Arg Glu Glu Val Arg Ala  
385 390 395

<210> 4

<211> 395

<212> PRT

<213> Artificial sequence

**<220>**

<223> Description of the artificial sequence: N-terminal his tagged

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Pro Tyr Leu Lys Asp Leu Gln Gln Asp Pro Leu Ala Val Leu Leu Ala  
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Trp Gly Arg Ala His Pro Arg Leu Phe Leu Pro Leu Pro Arg Phe Pro  
35 40 45

Leu Ala Leu Ile Phe Asp Pro Glu Gly Val Glu Gly Ala Leu Leu Ala  
50 55 60

Glu Gly Thr Thr Lys Ala Thr Phe Gln Tyr Arg Ala Leu Ser Arg Leu  
65 70 75 80

Thr Gly Arg Gly Leu Leu Thr Asp Trp Gly Glu Ser Trp Lys Glu Ala  
85 90 95

Arg Lys Ala Leu Lys Asp Pro Phe Leu Pro Lys Asn Val Arg Gly Tyr  
100 105 110

Arg Glu Ala Met Glu Glu Glu Ala Arg Ala Phe Phe Gly Glu Trp Arg  
115 120 125

Gly Glu Glu Arg Asp Leu Asp His Glu Met Leu Ala Leu Ser Leu Arg  
130 135 140

Leu Leu Gly Arg Ala Leu Phe Gly Lys Pro Leu Ser Pro Ser Leu Ala  
145 150 155 160

Glu His Ala Leu Lys Ala Leu Asp Arg Ile Met Ala Gln Thr Arg Ser  
 165 170 175  
 Pro Leu Ala Leu Leu Asp Leu Ala Ala Glu Ala Arg Phe Arg Lys Asp  
 180 185 190  
 Arg Gly Ala Leu Tyr Arg Glu Ala Glu Ala Leu Ile Val His Pro Pro  
 195 200 205  
 Leu Ser His Leu Pro Arg Glu Arg Ala Leu Ser Glu Ala Val Thr Leu  
 210 215 220  
 Leu Val Ala Gly His Glu Thr Val Ala Ser Ala Leu Thr Trp Ser Phe  
 225 230 235 240  
 Leu Leu Leu Ser His Arg Pro Asp Trp Gln Lys Arg Val Ala Glu Ser  
 245 250 255  
 Glu Glu Ala Ala Leu Ala Ala Phe Gln Glu Ala Leu Arg Leu Tyr Pro  
 260 265 270  
 Pro Ala Trp Ile Leu Thr Arg Arg Leu Glu Arg Pro Leu Leu Leu Gly  
 275 280 285  
 Glu Asp Arg Leu Pro Pro Gly Thr Thr Leu Val Leu Ser Pro Tyr Val  
 290 295 300  
 Thr Gln Arg Leu His Phe Pro Asp Gly Glu Ala Phe Arg Pro Glu Arg  
 305 310 315 320  
 Phe Leu Glu Glu Arg Gly Thr Pro Ser Gly Arg Tyr Phe Pro Phe Gly  
 325 330 335  
 Leu Gly Gln Arg Leu Cys Leu Gly Arg Asp Phe Ala Leu Leu Glu Gly  
 340 345 350  
 Pro Ile Val Leu Arg Ala Phe Phe Arg Arg Phe Arg Leu Asp Pro Leu  
 355 360 365  
 Pro Phe Pro Arg Val Leu Ala Gln Val Thr Leu Arg Pro Glu Gly Gly  
 370 375 380  
 Leu Pro Ala Arg Pro Arg Glu Glu Val Arg Ala  
 385 390 395

<210> 5

<211> 1188

<212> DNA

<213> Artificial sequence

<220>

<221> misc\_feature

<222> (1168)..(1185)

<223> His tag

<220>

<223> Description of the artificial sequence: N-terminal  
His-tagged

<220>

<221> CDS

<222> (1)..(1188)

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cag caa gat ccc ctc gcc gtc ctg ctg gcg tgg ggc cgg gcc cac ccc	96
Gln Gln Asp Pro Leu Ala Val Leu Leu Ala Trp Gly Arg Ala His Pro	
20 25 30	
cgg ctc ttc ctt ccc ctg ccc cgc ttc ccc ctg gcc ctg atc ttt gac	144
Arg Leu Phe Leu Pro Leu Pro Arg Phe Pro Leu Ala Leu Ile Phe Asp	
35 40 45	
ccc gag ggg gtg gag ggg gcg ctc ctc gcc gag ggg acc acc aag gcc	192
Pro Glu Gly Val Glu Gly Ala Leu Leu Ala Glu Gly Thr Thr Lys Ala	
50 55 60	
acc ttc cag tac cgg gcc ctc tcc cgc ctc acg ggg agg ggc ctc ctc	240
Thr Phe Gln Tyr Arg Ala Leu Ser Arg Leu Thr Gly Arg Gly Leu Leu	
65 70 75 80	
acc gac tgg ggg gaa agc tgg aag gag gcg cgc aag gcc ctc aaa gac	288
Thr Asp Trp Gly Glu Ser Trp Lys Glu Ala Arg Lys Ala Leu Lys Asp	
85 90 95	
ccc ttc ctg ccg aag aac gtc cgc ggc tac cgg gag gcc atg gag gag	336
Pro Phe Leu Pro Lys Asn Val Arg Gly Tyr Arg Glu Ala Met Glu Glu	
100 105 110	
gag gcc cgg gcc ttc ttc ggg gag tgg cgg ggg gag gag cgg gac ctg	384
Glu Ala Arg Ala Phe Phe Gly Glu Trp Arg Gly Glu Glu Arg Asp Leu	
115 120 125	
gac cac gag atg ctc gcc ctc tcc ctg cgc ctc ctc ggg cgg gcc ctc	432
Asp His Glu Met Leu Ala Leu Ser Leu Arg Leu Leu Gly Arg Ala Leu	
130 135 140	
ttc ggg aag ccc ctc tcc cca agc ctc gcg gag cac gcc ctt aag gcc	480
Phe Gly Lys Pro Leu Ser Pro Ser Leu Ala Glu His Ala Leu Lys Ala	

145	150	155	160	
ctg gac cgg atc atg gcc cag acc agg agc ccc ctg gcc ctc ctg gac				528
Leu Asp Arg Ile Met Ala Gln Thr Arg Ser Pro Leu Ala Leu Leu Asp	165	170	175	
ctg gcc gcc gaa gcc cgc ttc cgg aag gac cgg ggg gcc ctc tac cgc				576
Leu Ala Ala Glu Ala Arg Phe Arg Lys Asp Arg Gly Ala Leu Tyr Arg	180	185	190	
gag gcg gaa gcc ctc atc gtc cac ccg ccc ctc tcc cac ctt ccc cga				624
Glu Ala Glu Ala Leu Ile Val His Pro Pro Leu Ser His Leu Pro Arg	195	200	205	
gag cgc gcc ctg agc gag gcc gtg acc ctc ctg gtg gcg ggc cac gag				672
Glu Arg Ala Leu Ser Glu Ala Val Thr Leu Leu Val Ala Gly His Glu	210	215	220	
acg gtg gcg agc gcc ctc acc tgg tcc ttt ctc ctc ctc tcc cac cgc				720
Thr Val Ala Ser Ala Leu Thr Trp Ser Phe Leu Leu Leu Ser His Arg	225	230	235	240
ccg gac tgg cag aag cgg gtg gcc gag agc gag gag gcg gcc ctc gcc				768
Pro Asp Trp Gln Lys Arg Val Ala Glu Ser Glu Glu Ala Ala Leu Ala	245	250	255	
gcc ttc cag gag gcc ctg agg ctc tac ccc ccc gcc tgg atc ctc acc				816
Ala Phe Gln Glu Ala Leu Arg Leu Tyr Pro Pro Ala Trp Ile Leu Thr	260	265	270	
cgg agg ctg gaa agg ccc ctc ctc ctg gga gag gac cgg ctc ccc ccg				864
Arg Arg Leu Glu Arg Pro Leu Leu Leu Gly Glu Asp Arg Leu Pro Pro	275	280	285	
ggc acc acc ctg gtc ctc tcc ccc tac gtg acc cag agg ctc cac ttc				912
Gly Thr Thr Leu Val Leu Ser Pro Tyr Val Thr Gln Arg Leu His Phe	290	295	300	
ccc gat ggg gag gcc ttc cgg ccc gag cgc ttc ctg gag gaa agg ggg				960
Pro Asp Gly Glu Ala Phe Arg Pro Glu Arg Phe Leu Glu Glu Arg Gly	305	310	315	320
acc cct tcg ggg cgc tac ttc ccc ttt ggc ctg ggg cag agg ctc tgc				1008
Thr Pro Ser Gly Arg Tyr Phe Pro Phe Gly Leu Gly Gln Arg Leu Cys	325	330	335	
ctg ggg cgg gac ttc gcc ctc ctc gag ggc ccc atc gtc ctc agg gcc				1056
Leu Gly Arg Asp Phe Ala Leu Leu Glu Gly Pro Ile Val Leu Arg Ala	340	345	350	
ttc ttc cgc cgc ttc cgc cta gac ccc ctc ccc ttc ccc cgg gtc ctc				1104
Phe Phe Arg Arg Phe Arg Leu Asp Pro Leu Pro Phe Pro Arg Val Leu	355	360	365	
gcc cag gtc acc ctg agg ccc gaa ggc ggg ctt ccc gcg cgg cct agg				1152
Ala Gln Val Thr Leu Arg Pro Glu Gly Gly Leu Pro Ala Arg Pro Arg	370	375	380	

gag gag gtg cgg gcg cat cac cat cat cat cac tga  
 Glu Glu Val Arg Ala His His His His His His  
 385 390 395

1188

&lt;210&gt; 6

&lt;211&gt; 395

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

<223> Description of the artificial sequence: C-terminal  
 His-tagged

&lt;400&gt; 6

Met Lys Arg Leu Ser Leu Arg Glu Ala Trp Pro Tyr Leu Lys Asp Leu  
 1 5 10 15

Gln Gln Asp Pro Leu Ala Val Leu Leu Ala Trp Gly Arg Ala His Pro  
 20 25 30

Arg Leu Phe Leu Pro Leu Pro Arg Phe Pro Leu Ala Leu Ile Phe Asp  
 35 40 45

Pro Glu Gly Val Glu Gly Ala Leu Leu Ala Glu Gly Thr Thr Lys Ala  
 50 55 60

Thr Phe Gln Tyr Arg Ala Leu Ser Arg Leu Thr Gly Arg Gly Leu Leu  
 65 70 75 80

Thr Asp Trp Gly Glu Ser Trp Lys Glu Ala Arg Lys Ala Leu Lys Asp  
 85 90 95

Pro Phe Leu Pro Lys Asn Val Arg Gly Tyr Arg Glu Ala Met Glu Glu  
 100 105 110

Glu Ala Arg Ala Phe Phe Gly Glu Trp Arg Gly Glu Glu Arg Asp Leu  
 115 120 125

Asp His Glu Met Leu Ala Leu Ser Leu Arg Leu Leu Gly Arg Ala Leu  
 130 135 140

Phe Gly Lys Pro Leu Ser Pro Ser Leu Ala Glu His Ala Leu Lys Ala  
 145 150 155 160

Leu Asp Arg Ile Met Ala Gln Thr Arg Ser Pro Leu Ala Leu Leu Asp  
 165 170 175

Leu Ala Ala Glu Ala Arg Phe Arg Lys Asp Arg Gly Ala Leu Tyr Arg  
 180 185 190

Glu Ala Glu Ala Leu Ile Val His Pro Pro Leu Ser His Leu Pro Arg

195	200	205
Glu Arg Ala Leu Ser Glu Ala Val Thr Leu Leu Val Ala Gly His Glu		
210	215	220
Thr Val Ala Ser Ala Leu Thr Trp Ser Phe Leu Leu Leu Ser His Arg		
225	230	235 240
Pro Asp Trp Gln Lys Arg Val Ala Glu Ser Glu Glu Ala Ala Leu Ala		
	245	250 255
Ala Phe Gln Glu Ala Leu Arg Leu Tyr Pro Pro Ala Trp Ile Leu Thr		
	260	265 270
Arg Arg Leu Glu Arg Pro Leu Leu Leu Gly Glu Asp Arg Leu Pro Pro		
	275	280 285
Gly Thr Thr Leu Val Leu Ser Pro Tyr Val Thr Gln Arg Leu His Phe		
	290	295 300
Pro Asp Gly Glu Ala Phe Arg Pro Glu Arg Phe Leu Glu Glu Arg Gly		
305	310	315 320
Thr Pro Ser Gly Arg Tyr Phe Pro Phe Gly Leu Gly Gln Arg Leu Cys		
	325	330 335
Leu Gly Arg Asp Phe Ala Leu Leu Glu Gly Pro Ile Val Leu Arg Ala		
	340	345 350
Phe Phe Arg Arg Phe Arg Leu Asp Pro Leu Pro Phe Pro Arg Val Leu		
	355	360 365
Ala Gln Val Thr Leu Arg Pro Glu Gly Gly Leu Pro Ala Arg Pro Arg		
	370	375 380
Glu Glu Val Arg Ala His His His His His His		
385	390	395

&lt;210&gt; 7

&lt;211&gt; 30

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Description of the artificial sequence: PCR primer

&lt;400&gt; 7

cgaagctcat atgaagcgcc tttccctgag

30

&lt;210&gt; 8

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR primer

<400> 8

gcgaattcac gcccgcacct cctccctagg

30

<210> 9

<211> 42

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR primer

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42

<210> 10

<211> 42

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR primer

<400> 10

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42

<210> 11

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR primer

<400> 11

ccggaattca tgaagcgcct ttcctgagg

30

<210> 12

<211> 44

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR primer

<400> 12

ccaatgcatt gggtctgcag tcaggccgc acctcctccc tagg

44